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Review article

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A review on massive rise in multiple spike protein mutation of a corona virus sars-cov-2 - 501.v2 variant reported in UK

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ABSTRACT

A community of similar RNA viruses that cause diseases in mammals and birds are coronaviruses. They trigger respiratory tract infections in humans and birds that can range from moderate to lethal. SARS-CoV-2 Extreme Acute Respiratory Syndrome Coronavirus 2 was detected in China's e Wuhan province during September 2019. The total number of known positive cases has been estimated as of now (December 23, 2020) to be 78.2 million in all affected countries around the world and the death toll is 1,72 million. There are 10.2M positive cases in India and 146k people have died. The explanation behind the dramatic rise in Covid-19 cases in South and East England was discovered to be the latest SARS-CoV-2 strain at the end of December 2020. It is referred to as VUI (Variant Under Investigation) 202012/01, or the lineage B.1.1.7 is now originally recognised as Variant of Interest 202012/01 (VOC-202012/01). The purpose of his present work is to study the SARS-CoV-2 variant VOC-202012/01, VUI 202012/01 & 501.V2.

Keywords: SARS-CoV-2 , Variant, VOC, VUI.

INTRODUCTION

Human beings have evolved over the course of time to deal with situations and events that have threatened them at any stage of their lives. People all over the globe are facing a very similar situation because of a nanoscopic biological particle that has swept the universe by its stride. The most prominent topic over the last few months on a global scale has been the COVID pandemic and India was not an exception to its epidemic. COVID-19 is a recently described corona-virus disease. While several hypotheses have attempted to validate the argument that the global pandemic began in September 2019 as an outbreak in China's Wuhan province, the systematic authentication of the virus was not identified until November 2019. The causal agent was officially identified as the 2019 novel corona virus outbreak in December 2019, otherwise referred to as 2019-nCoV, which stands for novel corona virus.[1] The 2019 novel corona virus originated in China's Wuhan province and has become a global health problem issue. One of its own forms is the disorder which is thought to be zonotic in nature.

It was renamed SARS corona virus (severe acute respiratory syndrome corona virus) on 7 January 2020 by the International Committee on Virus Taxonomy on the basis of the type of clinical manifestation caused (ICTV). ICTV has indeed made the argument to validate the virus' position in causing a disease otherwise referred to as corona virus disease 2019 as COVID-19. The WHO (World Health Organization) then issued a call for a worldwide public health emergency to be instigated. In the sense of dire repercussions due to susceptible health systems, the WHO has declared the need for a worldwide health emergency. The World Health Organisation announced a global population health epidemic on 30 January 2020 that could compromise the health structure in many nations, leading to the outbreak of the infection.[2,3]

The prevalence of the disease was so fast that it quickly spread from China to other nations and was considered a serious pandemic that took lives. The total number of known positive cases has been estimated as of now (December 23, 2020) to be 78.2 million in all affected countries around the world and the death toll is 1,72 million. There are 10.2 million positive cases in India and 146,000 people have died.[4] As a matter of fact, by influencing their everyday practise, the pandemic has changed people's lifestyles. It may be accurately said that, in addition to biochemical manifestations, the pandemic has had a psychological effect on individuals. It may rightly be argued that the present situation has led human actions to be circumstantial. The new situation that has indeed caused people to acclimatise to a contrasting lifestyle distinct from what it used to be in the recent past might confirm this argument. The lack of an effective vaccine or treatment to combat the efficacy of the disease is one of the major problems related to the disease.

Virus Mutation

When a virus replicates or makes copies of itself, it sometimes changes a little bit. These changes are called "mutations". The virus with the new mutation(s) is called a "variant" of the original virus. Some viruses change fast and others more slowly. SARS-CoV-2, the virus which causes COVID-19, changes more slowly than others viruses such as HIV or influenza viruses. This is in part due to the fact that SARS-CoV-2 has an internal "proofreading mechanism" which corrects mistakes when it makes copies of itself. Most changes have little to no impact on the virus' properties. Occasionally, they result in a virus variant that is better adapted to its environment compared to the original virus. In that case, it can become dominant in a specific environment. This process of selection of successful variants is called "viral evolution" and this is a natural process all viruses go through. [5]

SARS-CoV-2 variant

The UK has faced a sharp spike in COVID-19 cases over the last couple of weeks. In South East England, this rise was pronounced, with the 14-day case notification rate increasing from 100 cases per 100 000 population in week 41/2020 to over 400 per 1,00,000 in week 50/2020. This rise resulted in an increased study of epidemiology and virology.

SARS-CoV-2 VUI 202012/01

A significant proportion (>50 percent) of cases were classified as belonging to a new single phylogenetic cluster using viral genome sequence data [6]. In the United Kingdom, this version is referred to as SARS-CoV-2 VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01). Overall, in the United Kingdom, about 5 to 10 percent of all COVID-19 cases are routinely sequenced, with sequencing coverage of about 4 percent in Kent, the most affected part of South East England. As of 13 December 2020, in England, 1,108 people were diagnosed with this virus variant, the earliest case being identified as of 20 September 2020. Overall, the observed rapid increase in COVID-19 cases was temporarily correlated with the appearance in November 2020 of a new variant in this region.

The identified cases of COVID-19 linked to the VUI 202012/01 version are concentrated in Kent and wider South East England, including the London and East England areas,

although there are reports that cases are more common throughout the United Kingdom, as well as limited numbers of cases found in other countries. As of 14 December 2020, 20 individuals from 4,733 sequenced samples obtained since 1 November were diagnosed with this virus variant in Wales. In addition, Denmark reported nine cases [7], the Netherlands reported one case [8], and the GISAID EpiCov database identified one case from Australia. The media confirmed that four cases in Belgium have been found in recent months [9].

VOC-202012/01

Variant of Concern 202012/01 (VOC-202012/01),[10] formerly known as the first Variant Under Investigation in December 2020 (VUI-202012/01)[11] and also as lineage B.1.1.7,[12][13] is a variant of SARS-CoV-2, the 2019 coronavirus disease (COVID-19) virus.[14] During the COVID-19 pandemic in the United Kingdom, the variant was first detected in October 2020 from a sample taken from the previous sample of COVID-19. It is associated with a substantial increase in the rate of COVID-19 infection in the United Kingdom; this increase is believed to be at least partially due to the N501Y modification within the receptor-binding domain of the spike glycoprotein that is necessary in human cells for binding to ACE2. [15]

In early December 2020, the latest mutation was identified, mixing genomic data with information that the rates of infection in Kent did not decline through national restrictions.[16] On 20 September 2020, the two earliest genomes belonging to the B.1.1.7 lineage were obtained in Kent and another in Greater London on 21 September 2020. These sequences (sequence accessions EPI ISL 601443 and EPI ISL 581117 respectively) have been submitted to the GISAID sequence database. There were 1623 genomes in the B.1.1.7 lineage as of 15 December. Of these, 519 were sampled in Greater London, 555 were sampled in Kent, 545 in other UK areas, including Scotland and Wales, and 4 were sampled in other countries. Since the variant was first identified in Kent, where it emerged can never be understood. Discovery in the UK may merely reflect that more sequencing is performed by the UK than by many other nations. It has been proposed that the variant could have originated in an immunocompromised individual chronically infected, allowing the virus a long period to replicate and evolve.[17]. 23 mutations are known as the VOC-202012/01 variant: 13 non-synonymous mutations, 4 deletions, and 6 synonymous mutations [18] (i.e., there are 17 mutations that modify proteins and 6 mutations that do not.

501.V2 Variant

The 501.V2 version, or simply 501.V2, is a mutated variant of the COVID-19-causing SARS-CoV-2 virus. The variant was first identified in South Africa and confirmed on 18 December 2020 by the health department of the country.[19] Scientists noted that the variant incorporates many mutations that make it easier to adhere to human cells due to three receptor-binding domain (RBD) mutations in the virus' spike glycoprotein, including N501Y[19][20] (change from asparagine (N) to tyrosioprotein). In Australia

and the UK, this specific mutation has also been identified.[19]

Epidemiology

Research into the properties of this new variant is underway, although there have been no findings of worse health conditions, increased mortality or especially affected populations to date. The cases with the VUI 202012/01 form are mostly found in people younger than 60 years, but this age demographic is similarly influenced by the rise in total COVID-19 cases in England. Preliminary modelling findings suggest that the existence of the new form in the Kent/South East England area is closely correlated with a rising occurrence of COVID-19. Cases have a median age of 41 years (range 11-71 years) among the VUI 202012/01 cases found in Wales, and are mostly concentrated in South Wales, where incidences are also increasing. [21]

The cluster ranges from the initial Wuhan strain by 29 nucleotide substitutions, higher than existing molecular clock estimates of about two substitutions per genome per month [22]. In the spike protein for the variant, the fraction of non-synonymous mutations is much greater than predicted from random mutations (27 percent of the 22 substitutions acquired since the Nextstrain clade 20B common ancestor are located in the S-gene, which comprises 13 percent of the viral genome, and all of these substitutions are nonsynonymous). Three sequences from Denmark and one from Australia, from samples obtained in November 2020, cluster with the UK version, most likely suggesting that, while the scale remains uncertain, foreign dissemination has occurred.

Spread

The first case was likely to be in London or Kent, United Kingdom, in mid-September 2020.[23] As of 13 December 2020, in almost 60 separate local authorities, 1,108 cases with this variant were found in the UK. These incidents were mainly in England's southeast. In Wales and Scotland, the variant has also been described. By November, the new variant was blamed for around a quarter of cases in the COVID-19 pandemic in London, and by December, it was a third.[24] In mid-December, it was calculated that VOC-202012/01 affected almost 60% of cases in London.[25] On 20 December 2020, the BBC announced that the World Health Organisation (WHO) had reported that nine cases of the new variant had been reported in Denmark .[26] Four were identified later on the same day in Belgium [27] and one in Italy.[28] The United Kingdom and Denmark

sequenced their SARS-CoV-2 cases at slightly higher rates than most others, [29] and it was thought likely that the variant would be observed later in additional countries. [30].

DISCUSSION

The strain is the product of several mutations in the SARS-CoV-2 novel coronavirus spike protein, as well as mutations in other RNA virus genomic areas. Preliminary research shows that it is more transmissible than versions that have been circulated before. In a region of the spike protein that binds to a central protein in the human cell, the ACE2 receptor, COG-UK named one of these mutations as "N501Y." This was a sign that, potentially, the improvements could lead to the virus becoming more contagious. Whole-genome sequencing, epidemiology and simulation evidence show that the current version is more readily spread than other strains. There is "no proof" that the variant is more likely to cause serious illness or mortality. "But we are pursuing investigations to better understand this," it added. It said that mortality is a "lagging indicator" and over the coming weeks it will "continually monitor this." Mutations in the spike protein will modify how the virus interacts with human cells, the portion of the virus that makes it contagious.

Phylogenetic research shows that the "cluster differs from the original Wuhan strain by 29 nucleotide substitutions," said the European Centre for Disease Prevention and Control. Three sequences from Denmark and one from Australia, from samples obtained in November 2020, cluster with the UK version, most likely suggesting that, while the scale remains uncertain, foreign dissemination has occurred. There is currently inadequate evidence to draw any inference about the underlying cause of increased transmissibility, age distribution and seriousness of the disease. Four deaths have been reported in about 1,000 incidents, but "further work is needed to compare this fatality rate with comparable data sets." [31]

CONCLUSION

The Covid-19 mutation discovered in the UK, which is also claimed to be extremely contagious again, can pose a threat to all countries' commercial, health and public health infrastructure. Time alone will say how our lives here in India will be affected by the virus. In addition, potential infections are expected to continue with viruses and organisms of pathogenic origin. Apart from curbing this epidemic, attempts should also be taken to formulate systematic steps to deter potential pathogenic outbreaks.

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